

## Exhibit B



## Conserved Domain Database

1/2

Protein: Nucleotide: Protein: Structure: CDD: Taxonomy: Help?

CD: pfam02877.8, PARP\_reg

PSSM-Id: 3371

Source: Pfam[US], Pfam[UK]

Description: Poly(ADP-ribose) polymerase, regulatory domain. Poly(ADP-ribose) polymerase catalyses the covalent attachment of ADP-ribose units from NAD<sup>+</sup> to itself and to a limited number of other DNA binding proteins, which decreases their affinity for DNA. Poly(ADP-ribose) polymerase is a regulatory component induced by DNA damage. The carboxyl-terminal region is the most highly conserved of the protein. Experiments have shown that a carboxyl 40 kDa fragment is still catalytically active.

Taxa: Eukaryota

References: 3 PubMed Links

Status: Alignment from source

Created: 11-Apr-2003

Aligned: 6 rows

PSSM: 134 columns

Representative: Consensus

Proteins: [Click here for CDART summary of Proteins containing pfam02877]

View 3D Structure

with Cn3D

using

Virtual Bonds

(To display structure, download Cn3D)

View Alignment

as

Hypertext

width

60

color

at

2.0 bits

Subset Rows

up to 10

of

the most diverse members

```

      10      20      30      40      50      60
consensus  .....|.....|.....|.....|.....|
3PAX       1  P...L...K...Y...D...L...T...T...T...G...A...Y...M...G...E...T...I...--D...E...I...D...L...L...S...F...S...R...Q...A...Y...V...L...E...Y...E...V... 58
gi_1353140 170  L...P...L...K...Y...D...L...T...T...T...G...A...Y...M...G...E...T...I...--D...E...I...D...L...L...S...F...S...R...Q...A...Y...V...L...E...Y...E...V... 66
gi_1709740 205  D...L...T...T...T...G...A...Y...M...G...E...T...I...--D...E...I...D...L...L...S...F...S...R...Q...A...Y...V...L...E...Y...E...V... 343
gi_548585   244  D...L...T...T...T...G...A...Y...M...G...E...T...I...--D...E...I...D...L...L...S...F...S...R...Q...A...Y...V...L...E...Y...E...V... 701
gi_1709741 287  P...L...K...Y...D...L...T...T...T...G...A...Y...M...G...E...T...I...--D...E...I...D...L...L...S...F...S...R...Q...A...Y...V...L...E...Y...E...V... 704

      70      80      90      100     110     120
consensus  .....|.....|.....|.....|.....|
3PAX       13  W...R...G...R...E...N...L...D...L...S...H...R...V...T...L...I...P...H...D...F...P...H...K...A...S...--L...I...U...H...Q...I...Q...A...N...P...Q...H...L...A...L...K...-E...I...E...V...A...S... 115
gi_1353140 190  W...R...G...R...E...N...L...D...L...S...H...R...V...T...L...I...P...H...D...F...P...H...K...A...S...--L...I...U...H...Q...I...Q...A...N...P...Q...H...L...A...L...K...-E...I...E...V...A...S... 123
gi_1709740 244  L...P...Y...D...F...L...E...L...S...G...E...Y...T...V...I...P...H...D...F...P...H...K...A...S...--L...I...U...H...Q...I...Q...A...N...P...Q...H...L...A...L...K...-E...I...E...V...A...S... 401
gi_548585   260  L...S...G...R...T...A...P...I...C...A...T...R...P...Y...T...L...I...S...H...R...V...T...L...I...P...H...D...F...P...H...K...A...S...--L...I...U...H...Q...I...Q...A...N...P...Q...H...L...A...L...K...-E...I...E...V...A...S... 756
gi_1709741 285  L...S...G...R...T...A...P...I...C...A...T...R...P...Y...T...L...I...S...H...R...V...T...L...I...P...H...D...F...P...H...K...A...S...--L...I...U...H...Q...I...Q...A...N...P...Q...H...L...A...L...K...-E...I...E...V...A...S... 761

      130
consensus  .....|.....|.....|.....|.....|
3PAX       118  L...D...L...T...A...S...I...K...E...I...S...L...E...P...H...Y...E... 124
gi_1353140 229  L...D...L...T...A...S...I...K...E...I...S...L...E...P...H...Y...E... 300
gi_1709740 402  L...S...V...H...G...L...Q...E...I...P...L...A...Y...H...Y...Q... 419
gi_548585   268  L...I...S...E...V...S...D...A...N...Y...L...O...H...N...Y...A... 277
gi_1709741 291  L...L...O...T...E...S...K...A...I...N...E...I...D...H...Y...D... 290

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